

CRF Errors Corrected by the STIC System. Branch

Serial Number: 10/038,010

+1) 05 90
 CRF Processing Date: 8/6/02 0730
 Edited by: DE
 Verified by: DE (STIC staff)

- ☐ Changed a file from non-ASCII to ASCII
- ☐ Changed the margins in cases where the sequence text was "wrapped" down to the next line.
- ☐ Edited a format error in the Current Application Data section, specifically: **ENTERED**
- ☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other _____
- ☐ Added the mandatory heading and subheadings for "Current Application Data".
- ☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.
- ☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically: _____
- ☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were: _____
- ☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited: _____
- ☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.
- ☐ Inserted colons after headings/subheadings. Headings edited included: _____
- ☐ Deleted extra, invalid, headings used by an applicant, specifically: _____
- ☒ Deleted: ☒ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file; ☐ page numbers throughout text; ☐ other invalid text, such as _____
- ☐ Inserted mandatory headings, specifically: _____
- ☐ Corrected an obvious error in the response, specifically: _____
- ☐ Edited identifiers where upper case is used but lower case is required, or vice versa.
- ☐ Corrected an error in the Number of Sequences field, specifically: _____
- ☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.
- ☐ Deleted **ending** stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: _____
- ☐ Other: _____

***Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.**



OIPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/038,010

DATE: 08/06/2002

TIME: 13:16:30

Input Set : A:\PTO.DC.txt

Output Set: N:\CRF4\08062002\J038010.raw

3 <110> APPLICANT: HYBRIGENICS
 4 Pierre, Legrain
 6 <120> TITLE OF INVENTION: Protein-protein interactions in adipocyte cells
 8 <130> FILE REFERENCE: B4767A
 10 <140> CURRENT APPLICATION NUMBER: US 10/038,010
 C--> 11 <141> CURRENT FILING DATE: 2002-07-23
 13 <150> PRIOR APPLICATION NUMBER: US 60/259,377
 14 <151> PRIOR FILING DATE: 2001-01-02
 16 <160> NUMBER OF SEQ ID NOS: 67
 18 <170> SOFTWARE: PatentIn version 3.1
 20 <210> SEQ ID NO: 1
 21 <211> LENGTH: 492
 22 <212> TYPE: DNA
 23 <213> ORGANISM: Homo sapiens
 25 <220> FEATURE:
 26 <221> NAME/KEY: gene
 27 <222> LOCATION: (1)..(492)
 28 <223> OTHER INFORMATION: Human Skp1 : Part of SCF (Skp1/Cullin/F-box) complexes which
 act
 29 as E3 Ubiquitin ligases.
 32 <400> SEQUENCE: 1
 33 atgccttcaa ttaagttgca gagttctgat ggagagatat ttgaagttga tgtggaaatt 60
 35 gccaaacaat ctgtaactat taagaccatg ttggaagatt tgggaatgga tgatgaagga 120
 37 gatgatgacc cagttcctct accaaatgtg aatgcagcaa tattaataaaa ggtcattcag 180
 39 tgggtgcaccc accacaagga tgaccctcct cctcctgaag atgatgagaa caaagaaaag 240
 41 cggacagatg atatccctgt ttgggaccaa gaattcctga aagttgacca aggaacactt 300
 43 tttgaactca ttctggctgc aaactactta gacatcaaag gtttgcttga tgttacatgc 360
 45 aagactgttg ccaatatgat caaggggaaa actcctgagg agattcgcaa gaccttcaat 420
 47 atcaaaaatg actttactga agaggaggaa gccacaggtac gcaaagagaa ccagtgggtg 480
 49 gaagagaagt ga 492
 52 <210> SEQ ID NO: 2
 53 <211> LENGTH: 163
 54 <212> TYPE: PRT
 55 <213> ORGANISM: Homo sapiens
 57 <220> FEATURE:
 W--> 58 <221> NAME/KEY: Skp1
 59 <222> LOCATION: (1)..(163)
 60 <223> OTHER INFORMATION:
 63 <400> SEQUENCE: 2
 65 Met Pro Ser Ile Lys Leu Gln Ser Ser Asp Gly Glu Ile Phe Glu Val
 66 1 5 10 15
 69 Asp Val Glu Ile Ala Lys Gln Ser Val Thr Ile Lys Thr Met Leu Glu
 70 20 25 30
 73 Asp Leu Gly Met Asp Asp Glu Gly Asp Asp Asp Pro Val Pro Leu Pro

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74          35          40          45
77 Asn Val Asn Ala Ala Ile Leu Lys Lys Val Ile Gln Trp Cys Thr His
78          50          55          60
81 His Lys Asp Asp Pro Pro Pro Pro Glu Asp Asp Glu Asn Lys Glu Lys
82 65          70          75          80
85 Arg Thr Asp Asp Ile Pro Val Trp Asp Gln Glu Phe Leu Lys Val Asp
86          85          90          95
89 Gln Gly Thr Leu Phe Glu Leu Ile Leu Ala Ala Asn Tyr Leu Asp Ile
90          100          105          110
93 Lys Gly Leu Leu Asp Val Thr Cys Lys Thr Val Ala Asn Met Ile Lys
94          115          120          125
97 Gly Lys Thr Pro Glu Glu Ile Arg Lys Thr Phe Asn Ile Lys Asn Asp
98          130          135          140
101 Phe Thr Glu Glu Glu Glu Ala Gln Val Arg Lys Glu Asn Gln Trp Cys
102 145          150          155          160
105 Glu Glu Lys

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109 <210> SEQ ID NO: 3

110 <211> LENGTH: 1917

111 <212> TYPE: DNA

112 <213> ORGANISM: Homo sapiens

114 <220> FEATURE:

115 <221> NAME/KEY: gene

116 <222> LOCATION: (1)..(1917)

117 <223> OTHER INFORMATION: Human Splicing Factor 1

120 <400> SEQUENCE: 3

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121 atggcgaccg gagcgaacgc cagcccggtg gacttcccaa gtaagaagcg gaagaggagc      60
123 cgctggaacc aagacacaat ggaacagaag acagtgattc caggaatgcc tacagttatt      120
125 ccccttggaac ttactcgaga acaagaaaga gcttatatag tgcaactgca gatagaagac      180
127 ctgactcgta aactgcgcac aggagacctg ggcatcccc ctaaccctga ggacagggtcc      240
129 ccttccccctg agcccatcta caatagcgag gggaagcggc ttaacaccgc agagttccgc      300
131 acccgcaaaa agctggaaga ggagcggcac aacctcatca cagagatggg tgcactcaat      360
133 ccggatttca agccacctgc agattacaaa cctccagcaa cacgtgtgag tgataaagtc      420
135 atgattccac aagatgagta ccagaaaatc aactttgtgg ggctgctcat cgggcccaga      480
137 gggaacaccc tgaagaacat agagaaggag tgcaatgcca agattatgat ccgggggaaa      540
139 gggctctgtga aagaaggga ggttgggcgc aaagatggcc agatgttgcc aggagaagat      600
141 gagccacttc atgccctggg tactgccaat acaatggaga acgtcaaaaa ggcagtggaa      660
143 cagataagaa acatcctgaa gcagggtatc gagactccag aggaccagaa tgatctacgg      720
145 aagatgcagc ttcgggagtt ggctcgctta aatgggaccc ttcgggaaga cgataacagg      780
147 atcttaagac cctggcagag ctgagagacc cgcagcatta ccaacaccac agtgtgtacc      840
149 aagtgtggag gggctggcca cattgcttca gactgtaaata tccaaaggcc tggatgatcct      900
151 cagtcagctc aggataaagc acggatggat aaagaatatt tgtccctcat ggctgaactg      960
153 ggtgaagcac ctgtcccagc atctgtgggc tccacctctg ggctgcccac cacaccctg      1020
155 gccagcgcac ctctcctgc tgctcccgcc aacaaccac ctccaccgct tctcatgtct      1080
157 accaccaga gccgccacc ctggatgaat tctggccctt cagagagtcg gccctaccac      1140
159 ggcatgcatg gaggtggtcc tgggtgggcc ggaggtggcc cccacagctt cccacacca      1200
161 ttaccagcc tgacaggtgg gcatggtgga catcccatgc agcacaacc caatggacc      1260
163 ccacccctt ggatgcagcc accaccacca ccgatgaacc agggcccca cctcctggg      1320
165 caccatggcc ctctccaat ggatcagtac ctgggaagta cgctgtggg ctctggggtc      1380
167 tatcgctgc atcaaggaaa aggtatgatg ccgccaccac ctatgggcat gatgccgccc      1440

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169 ccgccgccgc ctcccagtg ggcagccccc cccctccct ctggctctct tcccccatgg 1500
171 caacaacagc agcagcagcc tccgccaccc cctccgcccc gcagcagtat ggcttccagt 1560
173 acccccttgc catggcagca aaatacgacg actaccacca cgagcgctgg cacaggggtcc 1620
175 atcccgccat ggcaacagca gcaggcggct gccgcagctt ctccaggagc ccctcagatg 1680
177 caaggcaacc ccactatggt gcccctgccc cccgggggtcc agccgcctct gccgcctggg 1740
179 gcccctcccc ctccgcccgc tccaccgcct ggttccgccc gcatgatgat cctcccccgc 1800
181 ggccggcgatg gcccgagcca tgagagtga gactttccgc gccattggt gacccttcca 1860
183 ggcagacagc ctacgaacg cccctggtgg acaggatggt tcggcaaagc agcctga 1917

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186 <210> SEQ ID NO: 4

187 <211> LENGTH: 638

188 <212> TYPE: PRT

189 <213> ORGANISM: Homo sapiens

191 <220> FEATURE:

W--> 192 <221> NAME/KEY: Human Splicing Factor 1

193 <222> LOCATION: (1)..(638)

194 <223> OTHER INFORMATION:

197 <400> SEQUENCE: 4

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199 Met Ala Thr Gly Ala Asn Ala Thr Pro Leu Asp Phe Pro Ser Lys Lys
200 1 5 10 15
203 Arg Lys Arg Ser Arg Trp Asn Gln Asp Thr Met Glu Gln Lys Thr Val
204 20 25 30
207 Ile Pro Gly Met Pro Thr Val Ile Pro Pro Gly Leu Thr Arg Glu Gln
208 35 40 45
211 Glu Arg Ala Tyr Ile Val Gln Leu Gln Ile Glu Asp Leu Thr Arg Lys
212 50 55 60
215 Leu Arg Thr Gly Asp Leu Gly Ile Pro Pro Asn Pro Glu Asp Arg Ser
216 65 70 75 80
219 Pro Ser Pro Glu Pro Ile Tyr Asn Ser Glu Gly Lys Arg Leu Asn Thr
220 85 90 95
223 Arg Glu Phe Arg Thr Arg Lys Lys Leu Glu Glu Glu Arg His Asn Leu
224 100 105 110
227 Ile Thr Glu Met Val Ala Leu Asn Pro Asp Phe Lys Pro Pro Ala Asp
228 115 120 125
231 Tyr Lys Pro Pro Ala Thr Arg Val Ser Asp Lys Val Met Ile Pro Gln
232 130 135 140
235 Asp Glu Tyr Pro Glu Ile Asn Phe Val Gly Leu Leu Ile Gly Pro Arg
236 145 150 155 160
239 Gly Asn Thr Leu Lys Asn Ile Glu Lys Glu Cys Asn Ala Lys Ile Met
240 165 170 175
243 Ile Arg Gly Lys Gly Ser Val Lys Glu Gly Lys Val Gly Arg Lys Asp
244 180 185 190
247 Gly Gln Met Leu Pro Gly Glu Asp Glu Pro Leu His Ala Leu Val Thr
248 195 200 205
251 Ala Asn Thr Met Glu Asn Val Lys Lys Ala Val Glu Gln Ile Arg Asn
252 210 215 220
255 Ile Leu Lys Gln Gly Ile Glu Thr Pro Glu Asp Gln Asn Asp Leu Arg
256 225 230 235 240
259 Lys Met Gln Leu Arg Glu Leu Ala Arg Leu Asn Gly Thr Leu Arg Glu
260 245 250 255

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RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/038,010

DATE: 08/06/2002

TIME: 13:16:30

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Output Set: N:\CRF4\08062002\J038010.raw

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263 Asp Asp Asn Arg Ile Leu Arg Pro Trp Gln Ser Ser Glu Thr Arg Ser
264          260          265          270
267 Ile Thr Asn Thr Thr Val Cys Thr Lys Cys Gly Gly Ala Gly His Ile
268          275          280          285
271 Ala Ser Asp Cys Lys Phe Gln Arg Pro Gly Asp Pro Gln Ser Ala Gln
272          290          295          300
275 Asp Lys Ala Arg Met Asp Lys Glu Tyr Leu Ser Leu Met Ala Glu Leu
276 305          310          315          320
279 Gly Glu Ala Pro Val Pro Ala Ser Val Gly Ser Thr Ser Gly Pro Ala
280          325          330          335
283 Thr Thr Pro Leu Ala Ser Ala Pro Arg Pro Ala Ala Pro Ala Asn Asn
284          340          345          350
287 Pro Pro Pro Pro Ser Leu Met Ser Thr Thr Gln Ser Arg Pro Pro Trp
288          355          360          365
291 Met Asn Ser Gly Pro Ser Glu Ser Arg Pro Tyr His Gly Met His Gly
292          370          375          380
295 Gly Gly Pro Gly Gly Pro Gly Gly Gly Pro His Ser Phe Pro His Pro
296 385          390          395          400
299 Leu Pro Ser Leu Thr Gly Gly His Gly Gly His Pro Met Gln His Asn
300          405          410          415
303 Pro Asn Gly Pro Pro Pro Pro Trp Met Gln Pro Pro Pro Pro Pro Met
304          420          425          430
307 Asn Gln Gly Pro His Pro Pro Gly His His Gly Pro Pro Pro Met Asp
308          435          440          445
311 Gln Tyr Leu Gly Ser Thr Pro Val Gly Ser Gly Val Tyr Arg Leu His
312          450          455          460
315 Gln Gly Lys Gly Met Met Pro Pro Pro Pro Met Gly Met Met Pro Pro
316 465          470          475          480
319 Pro Pro Pro Pro Pro Ser Gly Gln Pro Pro Pro Pro Pro Ser Gly Pro
320          485          490          495
323 Leu Pro Pro Trp Gln Gln Gln Gln Gln Gln Pro Pro Pro Pro Pro Pro
324          500          505          510
327 Pro Ser Ser Ser Met Ala Ser Ser Thr Pro Leu Pro Trp Gln Gln Asn
328          515          520          525
331 Thr Thr Thr Thr Thr Thr Ser Ala Gly Thr Gly Ser Ile Pro Pro Trp
332          530          535          540
335 Gln Gln Gln Gln Ala Ala Ala Ala Ala Ser Pro Gly Ala Pro Gln Met
336 545          550          555          560
339 Gln Gly Asn Pro Thr Met Val Pro Leu Pro Pro Gly Val Gln Pro Pro
340          565          570          575
343 Leu Pro Pro Gly Ala Pro Pro Pro Pro Pro Pro Pro Pro Pro Gly Ser
344          580          585          590
347 Ala Gly Met Met Ile Pro Pro Arg Gly Gly Asp Gly Pro Ser His Glu
348          595          600          605
351 Ser Glu Asp Phe Pro Arg Pro Leu Val Thr Leu Pro Gly Arg Gln Pro
352          610          615          620
355 Gln Gln Arg Pro Trp Trp Thr Gly Trp Phe Gly Lys Ala Ala
356 625          630          635
359 <210> SEQ ID NO: 5

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RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/038,010

DATE: 08/06/2002

TIME: 13:16:30

Input Set : A:\PTO.DC.txt

Output Set: N:\CRF4\08062002\J038010.raw

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360 <211> LENGTH: 1173
361 <212> TYPE: DNA
362 <213> ORGANISM: mouse p53
364 <220> FEATURE:
365 <221> NAME/KEY: gene
366 <222> LOCATION: (1)..(1173)
367 <223> OTHER INFORMATION: mouse p53 : Tumour suppressor protein
370 <400> SEQUENCE: 5
371 atgactgcca tggaggagtc acagtcggat atcagcctcg agctccctct gagccaggag      60
373 acatttttcag gcttatggaa actacttcct ccagaagata tcctgccatc acctcactgc      120
375 atggacgata tgttgctgcc ccaggatggt gaggagtttt ttgaaggccc aagtgaagcc      180
377 ctccgagtgt caggagctcc tgcagcacag gaccctgtca ccgagacccc tgggccagcg      240
379 gccctgccc cagccactcc atggcccctg tcctcttttg tcccttctca aaaaacttac      300
381 cagggcaact atggcttcca cctgggcttc ctgcagtctg ggacagccaa gtctgttatg      360
383 tgcacgtact ctctccccc caataagcta ttctgccagc tggcgaagac gtgccctgtg      420
385 cagttgtggg tcagcgccac acctccagct gggagccgtg tccgcgccat ggccatctac      480
387 aagaagtcac agcacatgac ggaggtcgtg agacgctgcc cccaccatga gcgctgctcc      540
389 gatggtgatg gcctggctcc tcccagcat cttatccggg tgggaaggaa tttgtatccc      600
391 gagtatctgg aagacaggca gactttttgc cacagcgtgg tggtagctta tgagccaccc      660
393 gaggccggct ctgagtatac caccatccac tacaagtaca tgtgtaatag ctctgcatg      720
395 gggggcatga accgcccacc tacccttacc atcatcacac tgggaagactc cagtgggaac      780
397 cttctgggac gggacagctt tgaggttcgt gtttgtgcct gccctgggag agaccgccgt      840
399 acagaagaag aaaattttccg caaaaaggaa gtcctttgcc ctgaactgcc cccagggagc      900
401 gcaaagagag cgctgcccac ctgcacaagc gcctctcccc cgcaaaagaa aaaaccactt      960
403 gatggagagt atttcaccct caagatccgc gggcgtaaac gcttcgagat gttccgggag     1020
405 ctgaatgagg ccttagagtt aaaggatgcc catgctacag aggagtctgg agacagcagg     1080
407 gctcactcca gctacctgaa gaccaagaag ggccagtcta cttcccgcga taaaaaaaca     1140
409 atggtcaaga aagtggggcc tgactcagac tga                                     1173

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412 <210> SEQ ID NO: 6

413 <211> LENGTH: 390

414 <212> TYPE: PRT

415 <213> ORGANISM: mouse p53

417 <220> FEATURE:

W--> 418 <221> NAME/KEY: p53

419 <222> LOCATION: (1)..(390)

420 <223> OTHER INFORMATION:

423 <400> SEQUENCE: 6

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425 Met Thr Ala Met Glu Glu Ser Gln Ser Asp Ile Ser Leu Glu Leu Pro
426 1          5          10          15
429 Leu Ser Gln Glu Thr Phe Ser Gly Leu Trp Lys Leu Leu Pro Pro Glu
430          20          25          30
433 Asp Ile Leu Pro Ser Pro His Cys Met Asp Asp Leu Leu Leu Pro Gln
434          35          40          45
437 Asp Val Glu Glu Phe Phe Glu Gly Pro Ser Glu Ala Leu Arg Val Ser
438          50          55          60
441 Gly Ala Pro Ala Ala Gln Asp Pro Val Thr Glu Thr Pro Gly Pro Ala
442 65          70          75          80
445 Ala Pro Ala Pro Ala Thr Pro Trp Pro Leu Ser Ser Phe Val Pro Ser
446          85          90          95

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VERIFICATION SUMMARY
PATENT APPLICATION: US/10/038,010

DATE: 08/06/2002
TIME: 13:16:31

Input Set : A:\PTO.DC.txt
Output Set: N:\CRF4\08062002\J038010.raw

L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:58 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:2
L:192 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:4
L:418 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:6
L:604 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:8
L:794 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:10
L:901 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:12
L:1009 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:14
L:1061 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:16
L:1127 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:18
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L:1535 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:24
L:1601 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:26
L:1643 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:28
L:1681 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:30
L:1721 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:32
L:1767 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:34
L:1805 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:36
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L:2129 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:46
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L:3005 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:54
L:3215 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:56
L:3463 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:58
L:3579 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:60